

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 23, 2004, 18:53:56 ; Search time 12.3321 seconds

(without alignments)  
3525.629 Million cell updates/sec

Title: US-10-608-559-6

Perfect score: 2204

Sequence: 1 MVAHIGPGPIDEETPPAD.....QGILNALGQASAAVVSAGV 452

Scoring table: BLOSUM62

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR-78:\*  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2204	100.0	651	2 D72042	conserved hypotet
2	2204	100.0	651	2 E86581	CHLPP 76 kDa homol
3	2201	99.9	715	2 I40729	hypothetical 76X p
4	461.5	20.9	647	2 G71490	hypothetical prote
5	197	8.9	971	2 B90835	probable tail fibe
6	197	8.9	973	2 C85693	probable membrane
7	192.5	8.7	2055	2 T31110	extracellular matr
8	185.5	8.4	1822	2 S33441	BF protein - Strept
9	184	8.3	1122	2 G64887	probable tail fibe
10	181	8.2	2481	2 D90011	fimb protein (limp
11	176.5	8.0	545	2 E84327	Hcr7 transducer [l
12	176.5	8.0	545	2 E84327	Hcr14 transducer [
13	175	7.9	627	2 F84194	halobacterium tra
14	173	7.8	2271	2 F90073	hypothetical prote
15	172.5	7.8	1128	2 T30296	R27-2 protein - Tr
16	168.5	7.6	2232	2 T34434	hypothetical prote
17	168	7.6	993	2 C90072	hypothetical prote
18	164	7.4	6713	2 B89921	hypothetical prote
19	163.5	7.4	2155	2 AD2742	conserved hypotet
20	163.5	7.4	2155	2 C97523	transducer protein
21	160.5	7.3	536	2 A47190	transducer protein
22	160	7.3	536	2 E84318	Hcr1 transducer [i
23	160	7.3	536	2 E84318	Hcr1 transducer [i
24	158.5	7.2	4776	2 E95306	cell wall surface
25	157	7.1	641	2 C82306	methy]-accepting C
26	156	7.1	810	2 T46810	halobacterium tran
27	156	7.1	810	2 F84327	Hcr7 transducer [i
28	156	7.1	810	2 H89960	hypothetical prote
29	154.5	7.0	1238	2 T03465	probable exonuclea

30	154	7.0	5327	2 T13564	microtubule-associ
31	153.5	7.0	1147	2 T135781	hypothetical prote
32	153	6.9	860	2 T14650	tail fiber protein
33	153	6.9	978	2 T14968	phage lambda-relat
34	153	6.9	1365	2 T10822	impl protein - Myc
35	153	6.9	3624	2 AD0835	large repetitive D
36	152	6.9	892	2 T50985	related to transcr
37	150	6.8	990	2 T51618	nucleolar phosphop
38	150	6.8	1330	2 AF0351	probable autotrans
39	149.5	6.8	582	2 S24545	intermediate filam
40	149	6.8	778	2 T48897	transducer protein
41	149	6.8	1156	2 T34852	transducer secreted
42	149	6.8	1561	1 S06839	surface antigen gp
43	148.5	6.7	764	2 A84328	Hcr7 transducer [i
44	148.5	6.7	765	1 T44946	transducer protein
45	148.5	6.7	3890	2 C89921	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

D72042 conserved hypothetical protein CP0018 [imported] - Chlamydia pneumoniae (strains CM N/alterate names: chlpp 76 kDa homol) (Ct622); hypothetical protein CP00728

C/Species: Chlamydia pneumoniae; Chlamydia pneumoniae

C/Accession: D72042; D61623

R/Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J. Nature Genet. 21, 385-389, 1999

A/Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A/Reference number: A72000; PMID:99206606; PMID:10722368

A/Accession: D72042

A/Molecule type: DNA

A/Residues: 1-651 <ARN>

A/Cross-references: GB:AE001654; GB:AE001363; NID:94377031; PIDN:AD18867.1; PID:943770

A/Experimental source: strain CM1029

R/Read, T.D.; Brinkham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg

Nucleic Acids Res. 28, 1397-1406, 2000

A/Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.

A/Reference number: AB1500; PMID:20150255; PMID:10684935

A/Accession: D61623

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-651 <REA>

A/Cross-references: GB:AE002165; GB:AE002161; NID:G7188948; PIDN:AAF37914.1; PID:G71889

A/Experimental source: strain AR39, HU cells

C/Comment: This sequence was originally identified as homologous to part of a sequ

C/Genetics: PIR:H71490

C/Accession: CP00728; CP0016

Query Match 100.0%; Score 2204; DB 2; Length 651;

Best Local Similarity 100.0%; Pred. No. 7.2e-110; indels 0; gaps 0;

Matches 452; Conservative 0; Mismatches 0; indels 0; gaps 0;

1 MVAHIGPGPIDEETPPADLSAAGLEASAAKSAEARRIGAEXKPEKSTDEVERMSI 60

1 MVAHIGPGPIDEETPPADLSAAGLEASAAKSAEARRIGAEXKPEKSTDEVERMSI 60

1 MVAHIGPGPIDEETPPADLSAAGLEASAAKSAEARRIGAEXKPEKSTDEVERMSI 60



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 23, 2004, 10:53:56 / Search time 17.7616 Seconds  
(without alignments)  
3525.629 Million cell updates/sec

Title: US-10-608-559-2

Perfect score: 3187

Sequence: 1 MNPDIQGPIDETERTPPAD.....SIFQCVLVNIGSIXGTXIQ 651

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR.78.\*

1: PIR1.\*

2: PIR2.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	3187	100.0	651 2 D72042	conserved hypotet
2	3187	100.0	651 2 B8581	CHUPN 76 kDa homol
3	2205	69.2	715 2 I40729	hypothetical 76K P
4	899.5	28.2	647 2 G71490	hypothetical prote
5	233.5	7.3	2055 2 T31110	extracellular matr
6	232	7.3	1822 2 S33441	EF protein - Strept
7	223.5	7.0	2481 2 D90011	Fimb protein (Impo
8	221.5	7.0	971 2 B90835	probable tail fibre
9	221.5	7.0	973 2 C85693	probable membrane
10	220	6.9	6711 2 B89921	hypothetical prote
11	210	6.6	1122 2 G64887	probable tail fibre
12	210	6.6	2271 2 P90073	hypothetical prote
13	208.5	6.5	4776 2 E95205	cell wall surface
14	199	6.2	1365 2 T30822	Impr protein - Myc
15	196.5	6.2	1829 2 T24583	hypothetical prote
16	196.5	6.2	2232 2 T34434	hypothetical prote
17	192	6.0	1156 2 T34852	probable secreted
18	190.5	6.0	1063 2 D66731	hypothetical prote
19	189	5.9	2155 2 AD2742	conserved hypotet
20	189	5.9	2155 2 C97523	hypothetical prote
21	187	5.9	1147 2 T35781	hypothetical prote
22	186.5	5.9	1306 2 S25370	hypothetical prote
23	183	5.7	2186 2 H89960	MS2 protein - Yea
24	182.5	5.7	641 2 C82206	methy-accepting c
25	182.5	5.7	1238 2 T03465	probable exonuclea
26	182.5	5.7	2541 2 S11661	tailin - mouse
27	182	5.7	1269 2 F84730	probable myosin he
28	178.5	5.6	1566 2 A43607	cell surface anti
29	177	5.6	2090 2 S26058	probable transfor

10	176.5	5.5	545	2	E84327	Hcr7 transducer [1
31	176.5	5.5	545	2	T46811	halobacterial tran
32	176.5	5.5	3890	2	C89921	hypothetical prote
33	175.5	5.5	1104	2	S59310	probable membrane
34	175.5	5.5	5327	2	T13564	microtubule-associ
35	175	5.5	627	2	F84194	Hcr14 transducer [
36	175	5.5	891	2	G41662	130K surface exclu
37	175	5.5	1302	1	JC6009	surface-located me
38	173.5	5.4	1561	1	S06839	surface antigen sp
39	173	5.4	1072	2	A86827	hypothetical prote
40	173	5.4	2285	2	T12796	probable transglyc
41	172.5	5.4	1128	2	T30296	R27-2 protein - Tr
42	172.5	5.4	1601	2	AB1730	hypothetical prote
43	171.5	5.4	990	2	T51618	nucleolar phosphop
44	171	5.4	1787	2	AG1360	probable tape-meas
45	170.5	5.3	583	2	S67571	hypothetical prote

## ALIGNMENTS

RESULT 1  
D72042  
conserved hypothetical protein CP0018 [imported] - Chlamydia pneumoniae (strains CM  
N/Altemate names: chlpn 76 kDa homolog 1 (c622); hypothetical protein CP00728  
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae  
C/Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 11-May-2000  
C/Accession: D72042, D81623  
R/Kalman, S.; Mitchell, W.; Marathe, R.; Jammal, C.; Fan, J.; Olinger, L.; Grimwood, J.  
Nature Genet. 21, 385-389, 1999  
A/Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.  
A/Reference number: A72000; PMID:9206606; PMID:10192388  
A/Accession: D72042

A/Molecule type: DNA  
A/Residues: 1-651 <RNA>  
A/Cross-references: GB:AE001654; GB:AE001363; NID:94377031; PIDN:AD01867.1; PID:943770;  
A/Experimental source: strain CM029  
R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hick  
C.; Dodson, R.; Gwin, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salz  
Nucleic Acids Res. 28, 1397-1406, 2000  
A/Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR3  
A/Reference number: AB1500; PMID:20150255; PMID:10664935  
A/Accession: D81623

A/Status: Preliminary  
A/Molecule type: DNA  
A/Residues: 1-651 <RNA>  
A/Cross-references: GB:AE002165; GB:AE002161; NID:97188948; PIDN:AE37914.1; PID:971889;  
A/Experimental source: strain AR35, HL cells  
C/Comment: This sequence was originally identified as homologous to part of a sequence  
P/R:H71490).  
C/Genetics:  
A/Accession: CP00728; CP0018

Query Match  
Best Local Similarity 100.0%; Score 3187; DB 2; Length 651;  
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MNPDIQGPIDETERTPPADISAGLESAANKSAORINAKAEKPKSTDSVERSI 60  
1 MNPDIQGPIDETERTPPADISAGLESAANKSAORINAKAEKPKSTDSVERSI 60

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Db	361	EEAHNETASILMSGFRQMIHMFTEINTEPDSQAQCELLAQBARAKKAGDDSAAMALLADNAQ	420
Qy	421	ALPALGKAGQGGQGITNLALQILASAAVYAGVPPAAASIGSSVKOLYKTSKTSQSDYLT	480
Db	421	ALPALGKAGQGGQGITNLALQILASAAVYAGVPPAAASIGSSVKOLYKTSKTSQSDYLT	480
Qy	481	QISAGDAYKSLINDAYGRARNDATEDVINNVSTPALRSVPRAATERGEGKTDQALARY	540
Db	481	QISAGDAYKSLINDAYGRARNDATEDVINNVSTPALRSVPRAATERGEGKTDQALARY	540
Qy	541	ISGNSRTLDGVYSVSNLQVWQIISQSNPDANNEIRKQLTSATYKPPQFQYPVQLSND	600
Db	541	ISGNSRTLDGVYSVSNLQVWQIISQSNPDANNEIRKQLTSATYKPPQFQYPVQLSND	600
Qy	601	STQFKINKESLFAEGSRTAAEIKALSFEFNSLFTQQVLYNIGSYVSGYTLQ	651
Db	601	STQFKINKESLFAEGSRTAAEIKALSFEFNSLFTQQVLYNIGSYVSGYTLQ	651

RESULT 3  
 I40729  
 hypothetical 76k protein - Chlamydia pneumoniae (strain AR39)  
 C:\Species: Chlamydia pneumoniae, Chlamydia pneumoniae  
 Created: 16-Aug-1996 #sequence revision 16-Aug-1996 #text\_change 31-Mar-2000

Ortodoxobacteria pneumoniae (strain AR39)

hypothetical176k protein -/Chlamydogadus pneumoniae  
C/Species: Chlamydogadus pneumoniae, Chlamydia pneumoniae  
Accession revision 16-Aug-1996 #text change 31-Mar-2000

C;Date: 16-Aug-1996 #sequence\_version = 1.2  
C;Accession: I40729

R; Perez-Melgosa, M.; Kuo, C. Infect. Immun. 62, 880-886, 1994

A; Title: Isolation and characterization of a gene encoding a novel protein in *Escherichia coli*.  
A; Reference number: I40729; MUID: 94156481; PMID: 7509320

A: Accession: 140729  
R: Status: translated from GB/EMBL/DBJ

A: Molecule type: DNA

A;Residues: A/L23921; NID:g435961; PIDN:AAA23117.1; PID:g435962  
A;Cross-references: GB:L23921; strain AR-39

C;Comment: This is the hypothetical translation of a sequence that was reported as two

Query Match	Score	DB 2	Length
69.24;	2205;		715;
			98-100.

Best Local Similarity	99.64	Pred. NO. 1.35e+000
Matches 452	1	Mismatches 1
Conservative		Indels 0
		Gaps 0

1 WNPJGPGIDETERTPPADLSAGCLESAAKSAEAPORAGAEAKPKESKTDVERMSI 60

357 IUNYGPIDETETTPADLSAAGLEASANKSAEAOJLGAELAKPKESKTDSEVERMSI 316

JD  
ZJ  
67 1PBNVNAIWSADKTGIASSNSSSSSTRSADVDSITATAPTPPPETFDDYKTOAQAYDT 120

[illegible]

317 KSAVNALMSJAVNLSHOCNOBDE  
DB

0Y 121 IFTSTLADIQALNLSUDAVINNOVARDODDAAK 436

[illegible]

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437 ASDNCAIDLSIGKTSFDLLQALLQSVANNNRKAEELIKEMQDNREVFGRIPALAGSDVD

241 QTDATQIEKDGNAIRDAYFAGQNASGAVENAKSNNSISNIDSAKAIAITAKQIAEAC 50

497 QTDATATQIEODGNAIRDAYFAGONASGAVENANSNISISNDSAKKAIATAKTQIAEAO 55

301 KFPDPIQEAECWIAEKDLNKPADGSDVNPPTVGSKQGSIGSIRVMTL 360

557 KPEPDSPILOAEQWVIOAEKOLNINKPADGSDVPNECTTVGSKQGGSSIGSIRVSMLL 61E

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[illegible]

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 ORIGIN  
 Query Match 100.0%; Score 2156; DB 1; Length 10421;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AATAATCTTAAAGAGGCTCGCATTAATTAATTAAGAGCTTTTATTTTATTTT 60  
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 QY 61 AATAATCTTAAAGAGGCTTTTATTTTATTTTATTTTATTTTATTTTATTTT 120  
 Db 5073 AATAATCTTAAAGAGGCTTTTATTTTATTTTATTTTATTTTATTTTATTTT 5014  
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 Db 5013 AGGTCCTATAGAGGAAAGAGGAGCAACCTCCCGAGATCTTTCTGCTCAAGATTGA 4954  
 QY 181 GGGAGCTGAGCAATTAAGAGTGGGAAAGCTCAAGAAATAGCAGTCCGGAAGCTAAC 240  
 Db 4953 GGGAGCTGAGCAATTAAGAGTGGGAAAGCTCAAGAAATAGCAGTCCGGAAGCTAAC 4894  
 QY 241 TAAAGATCTAAGACCGATCTGTAGAGCGATGAGGATCTTGCTGCAAGTATGC 300  
 Db 4893 TAAAGATCTAAGACCGATCTGTAGAGCGATGAGGATCTTGCTGCAAGTATGC 4834  
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 Db 4773 CAGATCTGAGAGCTGAGCTCAACGACGACGACGACGACGACGACGACGACGAC 4714  
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 Db 4293 ACAGATAGAGAAAGATGAAATGAGATTAAGATGATATTTTGGAGAGCAAGACGTAG 4234  
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 Db 4233 TGGAGCTGTAGAAATGCTAATCTAATTAATTAATTAATTAATTAATTAATTAATTA 4174  
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 Db 4113 AATCTTCAAGAGGCAAAATGTAATTAAGCTGAGAAAGATCTTAAATATGCA 4054  
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 Db 4053 ACCTGAGATGTTCTGATGTTTCAAAATCAAGAACTACAGTTGAGAGCTCCAGACACA 3994  
 QY 1141 AGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200  
 Db 3993 AGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3934  
 QY 1201 CGCTTCATTTGATGCTGAGGTTTCGACAGATGATCAATGATCAATGAGAAATGC 1260  
 Db 3933 CGCTTCATTTGATGCTGAGGTTTCGACAGATGATCAATGATCAATGAGAAATGC 3874  
 QY 1261 TGAATCTCAAGCTGCGCAAGAGAGCTGAGAGCAAGATGAGAGAGAGAGAGAGAGAG 1320  
 Db 3873 TGAATCTCAAGCTGCGCAAGAGAGCTGAGAGCAAGATGAGAGAGAGAGAGAGAGAG 3814  
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 Db 3813 AGATGACAGTGTCTGACAGGCTGAGAGAGTCTCAAGAAAGCTTAAAGAGCTTAAAG 3754  
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 Db 3753 TAAAGCTGGGAAACAAAGGGGCAATCTCAATGCTTAAAGAGATGAGCTTCTGCTCT 3694  
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 Db 3693 TGTAGCGGAGAGTTCCTCCGCTGACAGAGTCTTAAGAGTCAATCTGTAAGACGCT 3634  
 QY 1501 TTAAAGAGCTCAAAATCTAAGAGTTCGATTAAGAAACAAGATACAGAGTATAGA 1560  
 Db 3633 TTAAAGAGCTCAAAATCTAAGAGTTCGATTAAGAAACAAGATACAGAGTATAGA 3574

